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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1371.68 Seconds
(without alignment) 12007.805 Million cell updates/sec

Title: US-09-807-933b-2

Perfect score: 1017

Sequence: 1 atgaagttatctactatgc.....caggtgtctcaagaataaa 1017

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	166.2	16.3	691	10	BE585661 EST#6PSP6
2	130.2	12.8	450	13	B1200729 c1f05f6.r
3	120.6	11.9	444	13	B1190695 B1190695
4	114.8	11.3	426	13	B1187295 B1187295
5	76.6	7.5	215	13	B1190568 B1190568
6	58.2	5.7	735	17	CNS04NSM AL299119 Tetradon

7	57.6	5.7	989	17	CNS02HA4	AL197365 Tetradon
8	56.6	5.6	289	13	B1191461	B1191461 k3g10f6.r
9	56.6	5.6	299	13	B1187393	B1187393 a3b03f6.r
10	56.6	5.6	494	17	FR0048073	AL444858 Fugu rubr
11	56.4	5.5	450	17	FR0025663	AL018519 F.rubrtipe
12	56.4	5.5	619	17	FR0047601	AL444386 Fugu rubr
13	56.2	5.5	736	13	B1357281	B1357281 REA3711.5
14	55.4	5.4	274	13	B1188678	B1188678 d2c10f6.r
15	55.4	5.4	280	13	B1190362	B1190362 h4n07f6.r
16	55.4	5.4	289	13	B1189728	B1189728 g1c06f6.r
17	55	5.4	501	17	FR0048173	AL444958 Fugu rubr
18	55	5.4	619	17	FR0006994	Z50754 F.rubrtipes
19	54.4	5.3	331	17	BH881398	BH881398 hv25c11.b
20	53.6	5.3	446	17	AZ155573	AZ155573 SP_0013_A
21	53.4	5.3	358	17	BH777605	BH777605 f2mb013f0
22	53.2	5.2	350	17	BH879665	BH879665 h47h12.g
23	53	5.2	218	17	BH875125	BH875125 hg83h02.g
24	53	5.2	311	9	AT002044	AT002044 AT002044
25	53	5.2	570	17	AZ149014	AZ149014 SP_0020_B
26	53	5.2	619	17	FR0047503	AL444288 Fugu rubr
27	53	5.2	824	17	AZ185454	AZ185454 SP_1005_A
28	52.6	5.2	895	17	AZ211584	AZ211584 SP_0156_B
29	52.6	5.2	914	17	AZ205202	AZ205202 SP_0100_A
30	52.2	5.1	1027	17	AZ206858	AZ206858 SP_0109_A
31	51.8	5.1	168	17	BH784725	BH784725 f2mb013f0
32	51.8	5.1	836	17	AQ411961	AQ411961 CpG0931A
33	51	5.0	204	17	BH882682	BH882682 hv38h10.g
34	50.8	5.0	627	17	BH179321	BH179321 014_P_01-
35	50.8	5.0	627	17	CNS07LFL	AL616275 T7 end of
36	50.8	5.0	933	17	AZ204694	AZ204694 SP_0100_A
37	50.6	5.0	976	17	CNS01FBX	AL141646 Anopheles
38	50.4	5.0	475	17	AZ145091	AZ145091 SP_0044_A
39	50.4	5.0	558	17	AZ146816	AZ146816 SP_0047_B
40	50.4	5.0	634	12	BG467984	BG467984 Na_L4_02G
41	50.4	5.0	686	12	BG468026	BG468026 Na_L4_02G
42	50.2	4.9	257	17	FR0026883	AL019712 F.rubrtipe
43	50	4.9	250	17	BH878991	BH878991 h85e08.b
44	49.8	4.9	392	17	FR0048008	AL444793 Fugu rubr
45	49.6	4.9	335	10	AM275677	AM275677 xp08e07.x

ALIGNMENTS

RESULT 1
LOCUS BE585661
DEFINITION EST#6PSP6_D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Trilicium aestivum cDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
ACCESSION BE585661
VERSION BE585661.1 GI:9838604
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Trilicium aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Trilicaceae; Trilicium.
REFERENCE 1 (bases 1 to 691)
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike cDNA library
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@afaf.ksu.edu
Sequence have been trimmed to remove vector sequence and low

REFERENCE 1 (bases 1 to 444)
 AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)
 COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included is the best homolog from a blastx search of Genbank nr 04-09-01 576 3e-59 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE KPEPCRSOR (EN)
 Seq primer: T3.

FEATURES
 source Location/Qualifiers
 1..444
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="13g10fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 85 a 127 c 92 g 140 t
 ORIGIN

Query Match 11.9%; Score 120.6; DB 13; Length 444;
 Best Local Similarity 63.1%; Pred. No. 6.9e-24;
 Matches 186; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 380 GTGTGCTCTGTGTAACGGTGTCACTACTGTTATGGAGTGTGTAAGGCTCTGTGA 439
 Db 150 GTGTGCTCTGTGTAAGTGGCACTTACTGATCTGGGACTGCTGCAAGCTTCTTCT 209
 Qy 440 GCTGCGCCGGTAAGGCCAATGTCACTTCTCTGCAAGTCTGTACAAGAATGTGTCA 499
 Db 210 CTGGAGCGGCAAGGCTAAAGTCAAGCGCCCTGCTGACTGTGACAAAGAATAAC 269
 Qy 500 CTGCCCTTAGTACAGCAATGCCCAAGTGTGTAAGGTGTGAACAGTTACATGTGA 559
 Db 270 CTATCACTAACCTGAACGCTGTCAACGGTGTGAGGGTGTGCTTATGTCTTCA 329
 Qy 560 ACGACAACCAACTTGGGCTGTAAAGCAACCTTGCCTATGCTGTGCA 619
 Db 330 CCAACTACTCCCGGGGCTGTCAACGACGACCTTTCGCTTCCGCTTACCAAGC 389
 Qy 620 TCAGTGTGTGTGAATCTCGCTGTGCTGTCTTCTTTTGGAACTTACTTTAC 674
 Db 390 TTGCTGTGTGTGAAGGCAAGCTGTGCTGTGCTTGTGCTTCAACTTCAAC 444

RESULT 4
 LOCUS B1187295 426 bp mRNA linear EST 10-JUL-2001
 DEFINITION B1187295.1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone alh1fs 5', mRNA sequence.
 ACCESSION B1187295
 VERSION B1187295.1 GI:14660974
 KEYWORDS EST.
 SOURCE Fusarium sporotrichioides.
 ORGANISM Fusarium sporotrichioides.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.
 REFERENCE 1 (bases 1 to 426)
 AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.

TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: alh1fs.fl
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included is the best homolog from a blastx search of Genbank nr 04-09-01 565 5e-58 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE KPEPCRSOR (EN)
 Seq primer: T3
 High quality sequence stop: 338.

FEATURES
 source Location/Qualifiers
 1..426
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="alh1fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 82 a 119 c 91 g 134 t
 ORIGIN

Query Match 11.3%; Score 114.8; DB 13; Length 426;
 Best Local Similarity 62.6%; Pred. No. 3.3e-22;
 Matches 179; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy 380 GTGTGCTCTGTGTAACGGTGTCACTACTGTTATGGAGTGTGTAAGGCTCTGTGA 439
 Db 140 GTGTGCTCTGTGTAAGTGGCACTTACTGATCTGGGACTGCTGCAAGCTTCTTCT 199
 Qy 440 GCTGCGCCGGTAAGGCCAATGTCACTTCTCTGCAAGTCTGTACAAGAATGTGTCA 499
 Db 200 CTGGAGCGGCAAGGCTAAAGTCAAGCGCCCTGCTGACTGTGACAAAGAATAAC 259
 Qy 500 CTGCCCTTAGTACAGCAATGCCCAAGTGTGTAAGGTGTGAACAGTTACATGTGA 559
 Db 260 CTATCACTAACCTGAACGCTGTCAACGGTGTGAGGGTGTGCTTATGTCTTCA 319
 Qy 560 ACGACAACCAACTTGGGCTGTAAAGCAACCTTGCCTATGCTGTGCA 619
 Db 320 CCAACTACTCCCGGGGCTGTCAACGACGACCTTGTACGGTTCCGCTTACCAAGC 379
 Qy 620 TCAGTGTGTGTGAATCTCGCTGTGCTGTCTTCTTTTGGAACT 665
 Db 380 TTGCTGTGTGTGAAGGCAAGCTGTGCTGTGCTTGTGCTTCAACTTCAAC 425

RESULT 5
 LOCUS B1190568 215 bp mRNA linear EST 10-JUL-2001
 DEFINITION B1190568.1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone 12el1fs 5', mRNA sequence.
 ACCESSION B1190568
 VERSION B1190568.1 GI:14664247
 KEYWORDS EST.
 SOURCE Fusarium sporotrichioides.
 ORGANISM Fusarium sporotrichioides.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.
 REFERENCE 1 (bases 1 to 215)
 AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)

COMMENT

Other ESTs: 12ellfs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability. Included is the best homolog from a blastx search of Genbank nr 04-09-01 363 7e-35 g|1170140|sp|P45659 PUTATIVE ENDOPLASMIC TYPE KPERCURSOR (EN)
Seq primer: T3
High quality sequence stop: 156.
Location/Qualifiers

FEATURES

source

1. 215
/organism="Fusarium sporotrichioides"

/strain="Tri 10"

/db_xref="taxon:5514"

/clone="12ellfs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into XhoI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT

44 a 61 c 53 g 56 t 1 others

ORIGIN

Query Match

Best Local Similarity 61.1%; Pred. No. 2.8e-11; Matches 124; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

412 TATTGGATTGCTGTAAAGGCTCTCTGTAAGTGGCCGGTAAGGCATGTCAGTTCCTT 471

1 TACTGGGAGCTGCTCAAGCCTCTTGTCTTGGAGCGCAAGCTAAAGTCAGGCCCTT 60

472 GTCAAGTCTGTAAAGATGATGTCACCTGCTTGTAGTACAGCAATGCCCAAGTGC 511

61 GCTGTGACTTGTGACACAAAGATTAACCTTATCACTAAGCAAGCGTGTGT 120

532 TGTAAAGGTGTAAAGTGTATGTAAGCAACCAAGCTTGGCTGTAAAGCAAC 591

121 GAGGGTGTGTCTTATGCTTATGTCACCAACTCTCCGCGGTGTCAACAGCAG 180

592 CTGGCTATGTTGCTGCTGC 614

181 CTGGCTAAGGTTTGTGCTGCTAC 203

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weisenbach, J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Unpublished
3 (bases 1 to 735)
Genoscope.
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES

source

1. 735
/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="123M05"

/note="Genoscope sequence ID : COBG123AG031P1-end : T7"

BASE COUNT

242 a 45 c 223 g 197 t 28 others

ORIGIN

Query Match

Best Local Similarity 53.6%; Pred. No. 1.2e-05; Matches 111; Conservative 4; Mismatches 92; Indels 0; Gaps 0;

202 AATAATCTCTGAAGTGTACAGAGACTACCACTGCTGTACAGAGACTACT 261

343 ACTTTTCTTCTGCTACTACTACTACTACTACTACTACTACTACTACTACT 284

262 ACCGCTGTCTATTAAGACACTACCTGCTCTGCTTAAGAGACTACAGCTGGCCAA 321

283 ACTACTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 224

322 GCTTCCACCCCTTCTACTACTACTACTACTACTACTACTACTACTACTACT 381

223 GCTACTACACTACTACTACTACTACTACTACTACTACTACTACTACTACT 164

382 GGTGCTCTGTGTACAGGTGTACTACT 408

163 GCTACTACACTACTACTACTACTACTACT 137

DB

QY

DB

QY

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QY

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QY

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QY

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QY

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QY

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weisenbach, J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Unpublished
3 (bases 1 to 735)
Genoscope.
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES

source

1. 735
/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="123M05"

/note="Genoscope sequence ID : COBG123AG031P1-end : T7"

BASE COUNT

242 a 45 c 223 g 197 t 28 others

ORIGIN

Query Match

Best Local Similarity 53.6%; Pred. No. 1.2e-05; Matches 111; Conservative 4; Mismatches 92; Indels 0; Gaps 0;

202 AATAATCTCTGAAGTGTACAGAGACTACCACTGCTGTACAGAGACTACT 261

343 ACTTTTCTTCTGCTACTACTACTACTACTACTACTACTACTACTACTACT 284

262 ACCGCTGTCTATTAAGACACTACCTGCTCTGCTTAAGAGACTACAGCTGGCCAA 321

283 ACTACTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 224

322 GCTTCCACCCCTTCTACTACTACTACTACTACTACTACTACTACTACTACT 381

223 GCTACTACACTACTACTACTACTACTACTACTACTACTACTACTACTACT 164

382 GGTGCTCTGTGTACAGGTGTACTACT 408

163 GCTACTACACTACTACTACTACTACTACT 137

DB

QY

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REFERENCE	3 (bases 1 to 989)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradon .
FEATURES	Location/Qualifiers
SOURCE	U. .989
	/organism="Tetradon nigroviridis"
	/db_xref="taxon:99883"
	/clone="139021"
	/clone_lib="G"
	/note="Genoscope sequence ID : COAG139M11P1-end : T7"
BASE COUNT	320 a 245 c 122 g 261 t 41 others
ORIGIN	
Query Match	5.7% Score 57.6; DB 17; Length 989;
Best Local Similarity	42.7% Pred. No. 2e-05;
Matches	205; Conservative 12; Mismatches 263; Indels 0; Gaps 0;
Oy	173 CTCATATCTCCCTCGAAGCAGTGGCATTAATCTTGTGAAGTGTGCACAAGAAGA 232
Db	121 CAAABACTCAACACACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 180
Oy	233 CTACCACTGTCTGCACAGAAAGACTACTACCGCTGTCAATAAAAGACTACACTGTCTC 292
Db	181 CTACTAATACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 240
Oy	293 CTGCTAAGAGACATCAACTGTTGGCAAGCTTCCACCCCTTCAACTCTAGCTTACT 352
Db	241 CTACTRCTACTACTACTACTACTACTACTGCTGTGTAATACTACTACTAATCTAATACTACTA 300
Oy	353 CCAAGCGCAATATATCCGCTGTCTGTGGTGGCTCTGTGAACGGTGTCACTACTCGTT 412
Db	301 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTG 360
Oy	413 ATTGGGATTTGCTGAAGGCTCTGTGTAGTCGGCCGGTAAGGCAATGTCAAGTTCCTGTG 472
Db	361 CTAAATACTACTACTAAATATCTACTACTACTACTACTACTACTACTACTACTACTACTACTA 420
Oy	473 TCAAGTCTGTAAACAAGATGTGTCTACTGCTCCCTTAGTGAACAGATGCCAAGTGTCT 532
Db	421 CTACTACTAAATAAATATATATATAATAATATATATATATATATATATATATATATATAT 480
Oy	533 GTAAACGGTGTGAACAGTACTATGTGTAAACGACCAACCTTGGGCTGTAAACGACCAAC 592
Db	481 CTCTCTACTACTACTAAT 540
Oy	593 TTGCTTAATGTTTGGCTGTCTGTGCATCAGTGTGTGTGTGAATCTGCTGTGTGTGT 652
Db	541 CCCCCGCTGCKRGGYGGTGTGTGGGGGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
RESULT 8	
LOCUS	Bi191461
DEFINITION	289 bp mRNA linear EST 10-JUL-2001
ACCESSION	Bi191461
VERSION	Bi191461.1
KEYWORDS	GI:14665140
SOURCE	EST.
ORGANISM	Fusarium sporotrichioides.
REFERENCE	Fusarium sporotrichioides.
AUTHORS	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; microsporid Hypocreales; Fusarium.
TITLE	1 (bases 1 to 289)
JOURNAL	Ren, O., Tag, A., Pego, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
	Analysis of a Fusarium sporotrichioides EST database
	Unpublished (2001)

COMMENT	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 333.6e-30 g[1170140]ep/P45699 PUTATIVE ENDOGUANINASE TYPE KRECURSOR (EN) Seq primer: T3 High quality sequence stop: 265.
FEATURES	Location/Qualifiers
SOURCE	1..289 /organism="Fusarium sporotrichioides" /strain="Tri 10" /db_xref="taxon:5514" /clone="k3g10fs" /clone_1fb="Fusarium sporotrichioides Tri 10 overexpressed cDNA library" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into XhoI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT	62 a 81 c 56 g 90 t
ORIGIN	
Query Match	5.6%; Score 56.6; DB 13; Length 289;
Best Local Similarity	60.9%; Pred. No. 2.1e-05;
Matches	92; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
OY	380 GTGTCGCCCTTGGTAACGGTGTCATCTGTATTGGAGTTGCTGTAAAGCCCTCCTGA 439
Db	133 GTGTCGCTTTGTGAAAGGCGCACCTCACTCATGATCTGGACTGTGCAAGCCTTCTGCT 192
OY	440 GCTGGCCCCGGTAAGGCCAATGTCAGTTCTCCTGCAGAGCTCTGTAAACAAGATGCTCA 499
Db	193 CTTGAGCGGCAAGGCTTAAGTAGTACGCCCCCTGCTGTGACTTGTGACAAACAAGATAAC 252
OY	500 CTGCGCCTTAAGTGACAGCAATGCCCAAGAATG 530
Db	253 CTATCACTAACCTGAACGCTGTCAACGGT 283
RESULT 9	B187393 299 bp mRNA linear EST 10-JUL-2001
LOCUS	B187393
DEFINITION	ab003fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone ab003fs 5', mRNA sequence.
ACCESSION	B187393
VERSION	B187393.1 GI:14661072
KEYWORDS	EST.
SOURCE	Fusarium sporotrichioides.
ORGANISM	Fusarium sporotrichioides Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium. 1 (bases 1 to 299)
REFERENCE	Ran, O., Tag, A., Peglow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M., and Roe, B. Analysis of a Fusarium sporotrichioides EST database Unpublished (2001)
TITLE	Other ESTs: ab003fs.f1
JOURNAL	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu
COMMENT	Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 339.1e-30 g[1170140]ep/P45699 PUTATIVE ENDOGUANINASE TYPE

FEATURES
source
KRECURSOR (EN)
Seq primer: T3
High quality sequence stop: 289.
Location/Qualifiers

1. 299
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone_id="a3b03fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into XhoI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 65 a 84 c 54 g 96 t
ORIGIN

Query Match 5.6%; Score 56.6; DB 13; Length 299;
Best Local Similarity 60.9%; Pred. No. 2.1e-05;
Matches 92; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Qy 380 GTGTGCTCTGTGTAACGGTGTCTACTGCTTATTGGGATGCTGTAAGCCCTCTGTA 439
Db 142 GTGTGCTCTGTGTAAGTGGCACTGCTACTGATGCTGGACTGCTGCAAGCTTCTTGTCT 201
Qy 440 GCTGAGCCCGTAAAGCCCAATGTCATGCTCTGTCAGTCTGTAACAAGATGCTGTA 499
Db 202 CTGTGACCGGCAAGGCTAAAGTCAAGCCGCTGCTGCTGCTGACCAACAAGATTAAC 261
Qy 500 CTGCCCTTAGTGACAGCAATGCCCAAGTGG 530
Db 262 CTATCACTAACCTAAGCCTCTCAACGGTTG 292

RESULT 10
FR0048073 494 bp DNA linear GSS 05-JAN-2001
LOCUS
DEFINITION Pugu rubripes GSS sequence, clone 263K15b08, genomic survey
sequence.

ACCESSION AL444858
VERSION AL444858.1 GI:12052694
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Takifugu rubripes

REFERENCE
AUTHORS Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Tetrapoda; Mammalia; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 494)

TITLE Direct Submission
JOURNAL Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS

COMMENT
DESCR: One pass dye-terminator sequencing of BAC (pBelobAC11) cloned
genomic sequence
The BACs can be obtained from <http://www.ingye.com>.
FEATURES
source
1. 494
Location/Qualifiers
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_id="263K15b08"
/clone_lib="BAC 263K15"

BASE COUNT 128 a 163 c 45 g 158 t
ORIGIN
Query Match 5.6%; Score 56.6; DB 17; Length 494;
Best Local Similarity 54.6%; Pred. No. 2.8e-05;
Matches 113; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 202 AATAAATCTTGAAGTCTCACAAGAGACTACCACTGCTGTCAAGAAAGACTACT 261
Db 156 ACTACTACTGTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 215
Qy 262 ACCGCTGCTCATTAAGAGACTACCACTGCTGCTGTAAGAGACTACTACTGTCGCA 321
Db 216 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 275
Qy 322 GCTTCACCCCTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 381
Db 276 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 335
Qy 382 GGTGCTCTGTGTAACGGTGTCACTACT 408
Db 336 ACTGCTGCTGTCTACTGCTGTCTACTACT 362

RESULT 11
FR0025683 450 bp DNA linear GSS 10-DEC-1997
LOCUS
DEFINITION F. rubripes GSS sequence, clone 154E17AC12, genomic survey sequence.
ACCESSION AL018519
VERSION AL018519.1 GI:2684887
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Takifugu rubripes

REFERENCE
AUTHORS Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Tetrapoda; Mammalia; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 450)
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umranta, Y.,
Williams, G. and Brenner, S.

TITLE Direct Submission
JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS

COMMENT
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.

FEATURES
source
1. 450
Location/Qualifiers
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_id="154E17AC12"
/clone_lib="cosmid 154E17"

BASE COUNT 96 a 140 c 64 g 144 t 6 others
ORIGIN

Query Match 5.5%; Score 56.4; DB 17; Length 450;
Best Local Similarity 55.0%; Pred. No. 3e-05;
Matches 111; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 207 ATCTTGAAGTCTCACAAGAGACTACCACTGCTGTCAAGAAAGACTACTACCC 266
Db 61 AACTCTACTAAGTCTACTACTACTACTACTACTACTACTACTACTACTACTACT 120
Qy 267 TGCTCATAAAAGACTACCACTGCTGCTGTAAGAGACTACCACTGTCGCAAGCTTC 326
Db 121 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 180
Qy 327 CACCCCTTCACTACTAGTCTGCTGCTGCAAGGCAATATTCGCGTGTCTGTGATGC 386
Db 181 TACGCTACTACTGCTACTGCTGCTGCTACTGCTACTATTACTACTGCTACTGCTG 240
Qy 387 CTCTGTAGCGGTGTCACTACT 408
Db 241 TGCTACTACTGCTACTACTACTACT 262

RESULT 12
PR0047601
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
COMMENT
FEATURES
BASE COUNT
ORIGIN

FR0047601 619 bp DNA 1linear GSS 05-JUN-2001
Fugu rubripes GSS sequence, clone 217A13IG11, genomic survey
sequence.
AL444386
AL444386.1 GI:12052222
GSS: genome survey sequence.
Takifugu rubripes.
Takifugu rubripes.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 619)
Clark, M.S.
Direct Submission
Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of BAC (pBelobAC11) cloned
genomic sequence
The BACs can be obtained from <http://www.incyte.com>.
Location/Qualifiers
1. 619
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="217A13IG11"
/clone_1ib="BAC 217A13"
102 a 172 c 92 g 177 t 76 others

Query Match 5.5%; Score 56.4; DB 17; Length 619;
Best Local Similarity 44.0%; Pred. No. 3.6e-05;
Matches 162; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

202 AATMAATCTTGTGAAAGTGTCTCAAGAAAGTACCACTGCTGCTCAAGAAAGTACT 261
49 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 108
262 ACCGCTGCTCATAAAGACTACTACTGCTGCTGCTCAAGAAAGTCAATGTTGCCAA 321
109 GCTGCTGCTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 168
322 GCTTCCACCCCTTCTACTACTACTACTACTACTACTACTACTACTACTACTACT 381
169 NCTNCTACNCTNCTACTACTACTACTACTACTACTACTACTACTACTACTACT 228
382 GGTGCTGTGTGAACGGTGTCTACTACTGTTATGGATTGCTGAAGGCTTCTGTAG 441
229 ACTACTACTNCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 288
442 TGGCCCGGTAAGCCCAATGTCACTTCTCCGTCAAGTCCGTGAACAAGATGCTG 501
289 ACTNCTNCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACT 348
502 GGCCTTAGTACAGCAATGCGCAAGTGGCTGAAGGCTGAAGCTTACATGTGTAA 561
349 ACNCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 408
562 GACCAACCA 569
409 TACTACTCA 416

RESULT 13
BI357281
LOCUS
DEFINITION

BI357281 736 bp mRNA 1linear EST 31-JUL-2001
RE43711.5prime RE Drosophila melanogaster normal.ized Embryo pFLC-1

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
COMMENT
FEATURES
BASE COUNT
ORIGIN

BI357281
BI357281.1 GI:15051735
EST.
fruit fly.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 736)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Friese, B., George
, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
Mungall, C.J., Nunoo, J., Paclebo, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and Rubin
, G.M.
BDGP/HM1 RE Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
hit genomic AB003419; arm:X [614512,913786]
estimated-cyto:1B12-1C4: 05/22/2001
plate: RE 437 row: A column: 11
High quality sequence stop: 703.
Location/Qualifiers
1. 736
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RE43711"
/clone_1ib="RE Drosophila melanogaster normalized Embryo
pFLC-1"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DHS-alpha Tona"
/note="Organ: embryo; Vector: pFLC; Site 1: XhoI; Site 2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

Query Match 5.5%; Score 56.2; DB 13; Length 736;
Best Local Similarity 59.9%; Pred. No. 4.4e-05;
Matches 94; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

173 CTCATGCTTCCCTGAGAGAGGCAATTAATCTTGTGAAGTGTCAAGAAAG 232
562 CTCATGCTTCCCTGAGAGAGGCAATTAATCTTGTGAAGTGTCAAGAAAG 621
233 CTACCACTGCTGTCAAGAAAGACTACTACCGCTGCTCATAAAGACTACCACTG 292
622 CTACTACCACTACTATACTACTACTACTACTACTACTACTACTACTACTACT 681
293 CTGCTAAGAACTACTACTGTTGCCAAGCTTCCAC 329
682 CTACTACCACTACTACTACTGCTGAGAAATACAC 718

RESULT 14
BI188678
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI188678 274 bp mRNA 1linear EST 10-JUL-2001
d2c10fs.r1 Fusarium sporotrichioides Tr1 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone d2c10fs 5', mRNA
sequence.
BI188678
BI188678.1 GI:14662357
EST.
Fusarium sporotrichioides.
Fusarium sporotrichioides

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota: Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Fusarium.
1 (bases 1 to 274)
Ren, Q., Tag, A., Peplov, A., Lai, H., Kupfer, C., Peterson, A., Beremand
, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
303.1e-27 g1|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 102.
Location/Qualifiers

FEATURES
source
1..274
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="d2c10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT
ORIGIN
62 a 80 c 49 g 83 t

Query Match 5.4%; Score 55.4; DB 13; Length 274;
Best Local Similarity 61.4%; Pred. No. 4.6e-05;
Matches 89; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 380 GTGTCCTCTGTGACGCTGCTACTGCTTATTTGGAGTTGCTGTAAGCCTCTGTA 439
DB 127 GTGTCCTCTGTGACGCTGCTACTGCTTATTTGGAGTTGCTGTAAGCCTCTGTA 186
QY 440 GCTGGCCCGGTAAAGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
DB 187 CTGGAGCGGCAAGGCTTAAAGTCAAGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 246
QY 500 CTGCCCTTAGTGAAGCAATGCCCA 524
DB 247 CTATCACTAACCTGAACGCTGCA 271

RESULT 15
BI190362 280 bp mRNA linear EST 10-JUL-2001
LOCUS h4h07fe.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone h4h07fe 5', mRNA
sequence.
ACCESSION BI190362
VERSION BI190362.1 GI:14664041
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 280)
AUTHORS Ren, Q., Tag, A., Peplov, A., Lai, H., Kupfer, C., Peterson, A., Beremand
, M. and Roe, B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other_ESTs: h4h07fe.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
303.1e-27 g1|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 261.
Location/Qualifiers

FEATURES
source
1..280
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="h4h07fe"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT
ORIGIN
60 a 79 c 53 g 88 t

Query Match 5.4%; Score 55.4; DB 13; Length 280;
Best Local Similarity 61.4%; Pred. No. 4.6e-05;
Matches 89; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 380 GTGTCCTCTGTGACGCTGCTACTGCTTATTTGGAGTTGCTGTAAGCCTCTGTA 439
DB 133 GTGTCCTCTGTGACGCTGCTACTGCTTATTTGGAGTTGCTGTAAGCCTCTGTA 192
QY 440 GCTGGCCCGGTAAAGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
DB 193 CTGGAGCGGCAAGGCTTAAAGTCAAGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 252
QY 500 CTGCCCTTAGTGAAGCAATGCCCA 524
DB 253 CTATCACTAACCTGAACGCTGCA 277

Search completed: June 17, 2003, 18:49:21
Job time: 1376.68 secs